

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/424,487A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☐ Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 ☐ Wrapped Aminos The amino acid number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 ☐ Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 ☐ Misaligned Amino Acid Numbering The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 ☐ Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 ☐ Variable Length Sequence(s) ☐ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
- 7 ☐ PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) ☐. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 8 ☐ Skipped Sequences (OLD RULES) Sequence(s) ☐ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 ☐ Skipped Sequences (NEW RULES) Sequence(s) ☐ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 10 ☐ Use of n's or Xaa's (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 ☐ Use of <213>Organism (NEW RULES) Sequence(s) ☐ are missing this mandatory field or its response.
- 12 ☒ Use of <220>Feature (NEW RULES) Sequence(s) 4,7-9 are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 ☐ PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/424,487A

DATE: 03/28/2001

TIME: 15:24:58

Input Set : N:\Crf3\Refhold\I424487A.raw

Output Set: N:\CRF3\03282001\I424487A.raw

Does Not Comply
Corrected Diskette Needed

1 <110> APPLICANT: CHOO, Yen
 2 KLUG, Aaron
 3 ISALAN, Mark
 4 <120> TITLE OF INVENTION: Nucleic Acid Binding Proteins
 5 <130> FILE REFERENCE: 71278/264975
 C--> 6 <140> CURRENT APPLICATION NUMBER: US/09/424,487A
 7 <141> CURRENT FILING DATE: 2000-02-29
 8 <150> PRIOR APPLICATION NUMBER: GB 9710809.6
 9 <151> PRIOR FILING DATE: 1997-05-23
 10 <150> PRIOR APPLICATION NUMBER: PCT/GB98/01512
 11 <151> PRIOR FILING DATE: 1998-05-26
 12 <160> NUMBER OF SEQ ID NOS: 17
 13 <170> SOFTWARE: PatentIn Ver. 2.1
 15 <210> SEQ ID NO: 1
 16 <211> LENGTH: 264
 17 <212> TYPE: DNA
 18 <213> ORGANISM: Artificial Sequence
 19 <220> FEATURE:
 20 <221> NAME/KEY: CDS
 21 <222> LOCATION: (1)..(264)
 22 <223> OTHER INFORMATION: Description of Artificial Sequence: encoding
 23 nucleic acid binding proteins
 24 <400> SEQUENCE: 1
 25 gca gaa gag aag cct ttt cag tgt cga atc tgc atg cgt aac ttc agc 48
 26 Ala Glu Glu Lys Pro Phe Gln Cys Arg Ile Cys Met Arg Asn Phe Ser
 27 1 5 10 15
 28 gat cgt act act ctt acc cgc cac acg agg acc cac aca ggc gag aag 96
 29 Asp Arg Thr Thr Leu Thr Arg His Thr Arg Thr His Thr Gly Glu Lys
 30 20 25 30
 31 cct ttt cag tgt cga atc tgc atg cgt aac ttc agc agg agc gat aac 144
 32 Pro Phe Gln Cys Arg Ile Cys Met Arg Asn Phe Ser Arg Ser Asp Asn
 33 35 40 45
 34 ctt acg aga cac cta agg acc cac aca ggc gag aag cct ttt cag tgt 192
 35 Leu Thr Arg His Leu Arg Thr His Thr Gly Glu Lys Pro Phe Gln Cys
 36 50 55 60
 37 cga atc tgc atg cgt aac ttc agg caa gct gat cat ctt caa gag cac 240
 38 Arg Ile Cys Met Arg Asn Phe Arg Gln Ala Asp His Leu Gln Glu His
 39 65 70 75 80
 40 cta aag acc cac aca ggc gag aag 264
 41 Leu Lys Thr His Thr Gly Glu Lys
 42 85
 44 <210> SEQ ID NO: 2
 45 <211> LENGTH: 88
 46 <212> TYPE: PRT
 47 <213> ORGANISM: Artificial Sequence
 48 <220> FEATURE:
 49 <223> OTHER INFORMATION: Description of Artificial Sequence: encoding

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50 nucleic acid binding proteins

51 <400> SEQUENCE: 2

52 Ala Glu Glu Lys Pro Phe Gln Cys Arg Ile Cys Met Arg Asn Phe Ser

53 1 5 10 15

54 Asp Arg Thr Thr Leu Thr Arg His Thr Arg Thr His Thr Gly Glu Lys

55 20 25 30

56 Pro Phe Gln Cys Arg Ile Cys Met Arg Asn Phe Ser Arg Ser Asp Asn

57 35 40 45

58 Leu Thr Arg His Leu Arg Thr His Thr Gly Glu Lys Pro Phe Gln Cys

59 50 55 60

60 Arg Ile Cys Met Arg Asn Phe Arg Gln Ala Asp His Leu Gln Glu His

61 65 70 75 80

62 Leu Lys Thr His Thr Gly Glu Lys

63 85

65 <210> SEQ ID NO: 3

66 <211> LENGTH: 18

67 <212> TYPE: PRT

68 <213> ORGANISM: Artificial Sequence

69 <220> FEATURE:

70 <223> OTHER INFORMATION: Description of Artificial Sequence: Nucleic acid

71 binding protein

72 <221> NAME/KEY: BINDING

73 <222> LOCATION: (1)..(18)

74 <223> OTHER INFORMATION: where X is any amino acid

75 <400> SEQUENCE: 3

W--> 76 Xaa Cys Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa His Xaa Xaa

77 1 5 10 15

W--> 78 Xaa His

80 <210> SEQ ID NO: 4

81 <211> LENGTH: 21

82 <212> TYPE: PRT

83 <213> ORGANISM: Artificial Sequence

84 <220> FEATURE:

85 <223> OTHER INFORMATION: Description of Artificial Sequence: where X is any

86 amino acid

87 <221> NAME/KEY: BINDING

88 <222> LOCATION: (1)..(21)

89 <400> SEQUENCE: 4

W--> 90 Xaa Cys Xaa Xaa Cys Xaa Xaa Phe Xaa Xaa Xaa Xaa Xaa Xaa Leu Xaa Xaa

91 1 5 10 15

W--> 92 His Xaa Xaa Xaa His

93 20

95 <210> SEQ ID NO: 5

96 <211> LENGTH: 26

97 <212> TYPE: PRT

98 <213> ORGANISM: Artificial Sequence

99 <220> FEATURE:

100 <223> OTHER INFORMATION: Description of Artificial Sequence: Consensus zinc

101 finger structure

This does not describe the genetic source of Artificial Sequence.

This goes on separate C2237 line

See item 12 on Error Summary sheet.

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Input Set : N:\Crf3\Refhold\I424487A.raw

Output Set: N:\CRF3\03282001\I424487A.raw

102 <221> NAME/KEY: BINDING
 103 <222> LOCATION: (1)..(26)
 104 <400> SEQUENCE: 5
 105 Pro Tyr Lys Cys Pro Glu Cys Gly Lys Ser Phe Ser Gln Lys Ser Asp
 106 1 5 10 15
 107 Leu Val Lys His Gln Arg Thr His Thr Gly
 108 20 25
 110 <210> SEQ ID NO: 6
 111 <211> LENGTH: 29
 112 <212> TYPE: PRT
 113 <213> ORGANISM: Artificial Sequence
 114 <220> FEATURE:
 115 <223> OTHER INFORMATION: Description of Artificial Sequence: Consensus
 116 zinc finger structure
 117 <221> NAME/KEY: BINDING
 118 <222> LOCATION: (1)..(29)
 119 <400> SEQUENCE: 6
 120 Pro Tyr Lys Cys Ser Glu Cys Gly Lys Ala Phe Ser Gln Lys Ser Asn
 121 1 5 10 15
 122 Leu Thr Arg His Gln Arg Ile His Thr Gly Glu Lys Pro
 123 20 25
 125 <210> SEQ ID NO: 7
 126 <211> LENGTH: 9
 127 <212> TYPE: PRT
 128 <213> ORGANISM: Artificial Sequence
 129 <220> FEATURE:
 130 <223> OTHER INFORMATION: Description of Artificial Sequence: where x
 131 denotes a given combination of the bases at
 132 interface between DNA subsites, and the four bases
 133 are equally represented at DNA position 3
 134 <221> NAME/KEY: BINDING
 135 <222> LOCATION: (1)..(9)
 136 <400> SEQUENCE: 7
 W--> 137 Gly Asn Xaa Xaa Cys Gly Gly Cys Gly
 138 1 5
 140 <210> SEQ ID NO: 8
 141 <211> LENGTH: 9
 142 <212> TYPE: PRT
 143 <213> ORGANISM: Artificial Sequence
 144 <220> FEATURE:
 145 <223> OTHER INFORMATION: Description of Artificial Sequence: where x
 146 denotes a known combination of the two bases at
 147 DNA positions 4X and 5X and there is equal
 148 probability of any of the four bases at DNA position 3
 149 <221> NAME/KEY: BINDING
 150 <222> LOCATION: (1)..(9)
 151 <400> SEQUENCE: 8
 W--> 152 Gly Asn Xaa Xaa Cys Gly Gly Cys Gly
 153 1 5

1) This statement does not explain Artificial Sequence;
 2) Xaa can only be a single amino acid, not a base.

same error

RAW SEQUENCE LISTING

DATE: 03/28/2001

PATENT APPLICATION: US/09/424,487A

TIME: 15:24:58

Input Set : N:\Crf3\Refhold\I424487A.raw

Output Set: N:\CRF3\03282001\I424487A.raw

155 <210> SEQ ID NO: 9
 156 <211> LENGTH: 9
 157 <212> TYPE: PRT
 158 <213> ORGANISM: Artificial Sequence
 159 <220> FEATURE:
 160 <223> OTHER INFORMATION: Description of Artificial Sequence: where X
 161 denotes a known combination of the two bases at
 162 DNA positions 4X and 5X
 163 <221> NAME/KEY: BINDING
 164 <222> LOCATION: (1)..(9)
 165 <400> SEQUENCE: 9
 W--> 166 Gly Cys Xaa Xaa Cys Gly Gly Cys Gly
 167 1 5
 169 <210> SEQ ID NO: 10
 170 <211> LENGTH: 28
 171 <212> TYPE: PRT
 172 <213> ORGANISM: Artificial Sequence
 173 <220> FEATURE:
 174 <223> OTHER INFORMATION: Description of Artificial Sequence: Zinc finger
 175 binding protein
 176 <221> NAME/KEY: BINDING
 177 <222> LOCATION: (1)..(28)
 178 <400> SEQUENCE: 10
 179 Phe Gln Cys Arg Ile Cys Met Arg Asn Phe Ser Asp Arg Ser Ser Leu
 180 1 5 10 15
 181 Thr Arg His Thr Arg Thr His Thr Gly Glu Lys Pro
 182 20 25
 184 <210> SEQ ID NO: 11
 185 <211> LENGTH: 28
 186 <212> TYPE: PRT
 187 <213> ORGANISM: Artificial Sequence
 188 <220> FEATURE:
 189 <223> OTHER INFORMATION: Description of Artificial Sequence: Zinc finger
 190 binding protein
 191 <221> NAME/KEY: BINDING
 192 <222> LOCATION: (1)..(28)
 193 <400> SEQUENCE: 11
 194 Phe Gln Cys Arg Ile Cys Met Arg Asn Phe Ser Asp Arg Ser His Leu
 195 1 5 10 15
 196 Thr Arg His Thr Arg Thr His Thr Gly Glu Lys Pro
 197 20 25
 199 <210> SEQ ID NO: 12
 200 <211> LENGTH: 27
 201 <212> TYPE: PRT
 202 <213> ORGANISM: Artificial Sequence
 203 <220> FEATURE:
 204 <223> OTHER INFORMATION: Description of Artificial Sequence: Zinc finger
 205 binding protein
 206 <221> NAME/KEY: BINDING

same
err

RAW SEQUENCE LISTING

DATE: 03/28/2001

PATENT APPLICATION: US/09/424,487A

TIME: 15:24:58

Input Set : N:\Crf3\Refhold\I424487A.raw

Output Set: N:\CRF3\03282001\I424487A.raw

207 <222> LOCATION: (1)..(27)
 208 <400> SEQUENCE: 12
 209 Phe Gln Cys Arg Ile Cys Met Arg Asn Phe Ser Asp Arg Ser Asn Leu
 210 1 5 10 15
 211 Thr Arg His Thr Arg Thr His Thr Gly Glu Lys
 212 20 25
 214 <210> SEQ ID NO: 13
 215 <211> LENGTH: 9
 216 <212> TYPE: PRT
 217 <213> ORGANISM: Artificial Sequence
 218 <220> FEATURE:
 219 <223> OTHER INFORMATION: Description of Artificial Sequence: Zinc finger
 220 binding protein
 221 <221> NAME/KEY: BINDING
 222 <222> LOCATION: (1)..(9)
 223 <400> SEQUENCE: 13
 224 Ala Gly Ala Gly Ala Gly Cys Thr Cys
 225 1 5
 227 <210> SEQ ID NO: 14
 228 <211> LENGTH: 8
 229 <212> TYPE: PRT
 230 <213> ORGANISM: Artificial Sequence
 231 <220> FEATURE:
 232 <223> OTHER INFORMATION: Description of Artificial Sequence: 8bp
 233 palindromic sequence which is bound and cleaved by
 234 the restriction endonuclease NotI
 235 <221> NAME/KEY: BINDING
 236 <222> LOCATION: (1)..(8)
 237 <400> SEQUENCE: 14
 238 Gly Cys Gly Gly Cys Cys Gly Cys
 239 1 5
 241 <210> SEQ ID NO: 15
 242 <211> LENGTH: 9
 243 <212> TYPE: PRT
 244 <213> ORGANISM: Artificial Sequence
 245 <220> FEATURE:
 246 <223> OTHER INFORMATION: Description of Artificial Sequence: zinc finger
 247 binding protein
 248 <221> NAME/KEY: BINDING
 249 <222> LOCATION: (1)..(9)
 250 <400> SEQUENCE: 15
 251 Gly Cys Gly Gly Cys Cys Gly Cys Gly
 252 1 5
 254 <210> SEQ ID NO: 16
 255 <211> LENGTH: 8
 256 <212> TYPE: PRT
 257 <213> ORGANISM: Artificial Sequence
 258 <220> FEATURE:
 259 <223> OTHER INFORMATION: Description of Artificial Sequence: NotI

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/424,487A

DATE: 03/28/2001

TIME: 15:24:59

Input Set : N:\Crf3\Refhold\I424487A.raw

Output Set: N:\CRF3\03282001\I424487A.raw

L:6 M:270 C: Current Application Number differs, Wrong Format
L:76 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:78 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:90 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:92 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:137 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:152 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:166 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9